CLAIMS

1. A method for detecting an HBV-derived nucleic acid target sequence in a sample, said method comprising subjecting the sample to denaturing conditions to yield single stranded forms of said target sequence, contacting the denatured sample with a set of primers comprising at least two primers wherein at least one primer is capable of hybridizing to one strand of said target sequence and wherein at least one other primer is capable of hybridizing to a strand complementary to said first mentioned strand and wherein said primers are extendable from their 3' termini to form an extension product complementary to the strand to which each of said primers has hybridized and subjecting the sample to conditions to facilitate amplification to generate an amplified product comprising complementary extension products and then detecting for the presence of the amplification product wherein the presence of said amplified product is indicative of said HBV-derived nucleic acid target sequence.

2. A method according to Claim 1 wherein the primers hybridize to regions corresponding to or flanking a nucleotide sequence within or part of the nucleotide sequence encoding HBsAg.

3. A method according to Claim 2 wherein the primers hybridize to regions corresponding to or flanking a conserved nucleotide sequence within a part of the nucleotide sequence encoding HBsAg.

4. A method according to Claim 1 or 2 or 3 further comprising first subjecting the sample to reverse transcription conditions to yield single or double stranded cDNA molecules from HBV-derived mRNA.

5. A method according to Claim 1 wherein one of said primers is labelled with a reporter molecule capable of giving an identifiable signal and the other of said primers is labelled with a capturable moiety.

6. A method for detecting an HBV-derived DNA target sequence in a sample, said method comprising introducing said sample to a reaction vessel having a primer immobilized to a solid support and a second primer in solution phase wherein both primers are capable of hybridizing to a complementary nucleotide sequence on complementary single strands of HBV-derived DNA in a region within, proximal or adjacent to a conserved region on the HBV genome and wherein the solution phase primer is labelled

with a reporter molecule capable of giving an identifiable signal, subjecting the reaction vessel to conditions to facilitate amplification and then detecting the presence of the identifiable signal wherein the presence of said signal is indicative of the presence of HBV-derived DNA.

7. A method for detecting one or more HBV-derived DNA target sequences from the same or different strains or variants of HBV, said method comprising contacting a sample putatively comprising HBV-derived DNA in single stranded form with two or more primers immobilized individually or in an array to a solid support in a reaction vessel wherein the reaction vessel further comprises solution phase primers having an partner immobilized to the solid support wherein the immobilized primer and its solution phase partner primer are capable of amplifying under amplifying conditions a region of HBV-derived DNA wherein the solution phase primer carries a reporter molecule capable of giving an identifiable signal such that the presence of a signal at a defined location on the solid support enables the identification of a particular HBV isolate or variant.

8. An array of two or more oligonucleotide primers immobilized to a solid support, said primers capable of hybridizing to a complementary nucleotide sequence from HBV-derived DNA.

9. An array according to Claim 8 wherein the array is defined by the formula $a_1a_2 \ldots a_n$, having coordinates on the matrix (x_1y_1), (x_2y_2) ... (x_ny_n) wherein $a_1a_2 \ldots a_n$ represent the same or different oligonucleotides totalling n oligonucleotides and each oligonucleotide is definable by grid coordinates (x_1y_1), (x_2y_2) ... (x_ny_n) and wherein the oligonucleotides have amplification partners defined by $b_1b_1 \ldots b_n$ such that oligonucleotides a_1b_1, a_2b_2 ... a_nb_n are capable of hybridizing to complementary strands of HBV-derived DNA wherein the intervening DNA comprises a sequence of nucleotides conserved between two or more HBV variants, such as HBsAg variants, wherein said matrix is useful for detecting particular HBV agents defined by carrying the conserved amplification region of said HBV-derived DNA.

10. A method according to Claim 1 wherein the primers are selected from <400>1 and <400>2 or primers having at least 70% similarity thereto or primers capable of hybridizing to <400> 1 or <400>2 under low stringency conditions.

11. An HBV variant, generally in isolated form, which HBV variant is identified by a method of detecting an HBV-derived nucleic acid target sequence, said method

comprising subjecting the sample to denaturing conditions to yield single stranded forms of said target sequence, contacting the denatured sample with a set of primers comprising at least two primers wherein at least one primer is capable of hybridizing to one strand of said target sequence and wherein at least one other primer is capable of hybridizing to a strand complementary to said first mentioned strand and wherein said primers are extendable from their 3' termini to form an extension product complementary to the strand to which each of said primers has hybridized and subjecting the sample to conditions to facilitate amplification to generate an amplified product comprising complementary extension products and then detecting for the presence of the amplification product wherein the presence of said amplified product is indicative of said HBV-derived nucleic acid target sequence and then isolating said HBV so detected.

12. A means for identifying expression products such as a peptide, polypeptide or protein useful as immunological markers and/or for generating immunoglobulins for use in diagnosis and/or therapy.